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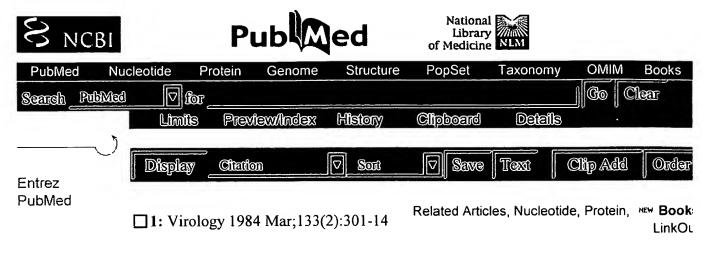
variation /note="g in KOS; a in mutant tsJ20" variation 1676 /note="c in KOS; t in mutant tsJ12" BASE COUNT 717 a 1286 c 1128 q 627 t ORIGIN 295 bp upstream of XhoI site; left half of BamHI-G frag at .370 mu. 1 gtcaacgggc ccctctttga tcactccacc cacagcttcg cccagccccc caacaccgcg 61 ctgtattaca gcgtcgagaa cgtggggctc ctgccgcacc tgaaggagga gctcgcccgg 121 ttcatcatgg gggcggggg ctcgggtgct gattgggccg tcagcgaatt tcagaggttt 181 tactgttttg acggcatttc cggaataacg cccactcagc gcgccgcctg gcgatatatt 241 cgcgagctga ttatcgccac cacactcttt gcctcggtct accggtgcgg ggagctcgag 301 ttgcgccgcc cggactgcag ccgcccgacc tccgaaggtc gttaccgtta cccgcccggc 361 gtatatetea egtaegaete egaetgteeg etggtggeea tegtegagag egeeceegae 421 ggctgtatcg gccccggtc ggtcgtggtc tacgaccgcg acgttttctc gatcctctac 481 tcggtcctcc agcacctcgc ccccaggcta cctgacgggg ggcacgacgg gcccccgtag 541 tecegecatg caecagggeg ecceetegtg ggggegeegg tggttegteg tatgggeget 601 cttggggttg acgctggggg tcctggtggc gtcggcggct ccgacttccc ccggcacgcc 661 tggggtcgcg gccgcgaccc aggcggcgaa cgggggccct gccactccgg cgccgccgcc 721 ccttggcgcc gccccaacgg gggacccgaa accgaagaag aacaaaaaac cgaaaaaccc 781 aacgccacca cgccccgccg gcgacaacgc gaccgtcgcc gcgggccacg ccaccctgcg 841 cgagcacctg cgggacatca aggcggagaa caccgatgca aacttttacg tgtgcccacc 901 ccccacgggc gccacggtgg tgcagttcga gcagccgcgc cgctgcccga cccggcccga 961 gggtcagaac tacacggagg gcatcgcggt ggtcttcaag gagaacatcg ccccgtacaa 1021 gttcaaggcc accatgtact acaaagacgt caccgtttcg caggtgtggt tcggccaccg 1081 ctactcccag tttatgggga tctttgagga ccgcgccccc gtccccttcg aggaggtgat 1141 cgacaagatc aacgccaagg gggtctgtcg gtccacggcc aagtacgtgc gcaacaacct 1201 ggagaccacc gcgtttcacc gggacgacca cgagaccgac atggagctga aaccggccaa 1261 cgccgcgacc cgcacgagcc ggggctggca caccaccgac ctcaagtaca acccctcgcg 1321 ggtggaggcg ttccaccggt acgggacgac ggtaaactgc atcgtcgagg aggtggacgc 1381 gcgctcggtg tacccgtacg acgagtttgt gctggcgact ggcgactttg tgtacatgtc 1441 cccgttttac ggctaccggg aggggtcgca caccgaacac accacgtacg ccgccgaccg 1501 cttcaagcag gtcgacggct tctacgcgcg cgacctcacc accaaggccc gggccacggc 1561 geogaecace eggaacetge teaegaecee caagtteaee gtggeetggg aetgggtgee 1621 aaagegeeeg teggtetgea eeatgaeeaa gtggeaggaa gtggaegaga tgetgegete 1681 cgagtacggc ggctccttcc gattctcctc cgacgccata tccaccacct tcaccaccaa 1741 cctgaccgag tacccgctct cgcgcgtgga cctgggggac tgcatcggca aggacgcccg 1801 cgacgccatg gaccgcatct tcgcccgcag gtacaacgcg acgcacatca aggtgggcca 1861 geogeagtae taccaggeea atgggggett tetgategeg taccageece tteteageaa 1921 cacgctcgcg gagctgtacg tgcgggaaca cctccgagag cagagccgca agcccccaaa 1981 ccccacgccc ccgccgcccg gggccagcgc caacgcgtcc gtggagcgca tcaagaccac 2041 ctcctccatc gagttcgccc ggctgcagtt tacgtacaac cacatacagc gccatgtcaa 2101 cgatatgttg ggccgcgttg ccatcgcgtg gtgcgagcta cagaatcacg agctgaccct 2161 gtggaacgag gcccgcaagc tgaaccccaa cgccatcgcc tcggtcaccg tgggccggcg 2221 ggtgagcgcg cggatgctcg gcgacgtgat ggccgtctcc acgtgcgtgc cggtcgccgc 2281 ggacaacgtg atcgtccaaa actcgatgcg catcagctcg cggcccgggg cctgctacag 2341 ccgcccctg gtcagctttc ggtacgaaga ccagggcccg ttggtcgagg ggcagctggg 2401 ggagaacaac gagctgcggc tgacgcgcga tgcgatcgag ccgtgcaccg tgggacaccg 2461 gegetaette acetteggtg ggggetaegt gtaettegag gagtaegegt acteceaeca

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     3721 ggccccggcc tccgcgttgg atgctccggt tgggatcc
11
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Revised: October 24, 2001.

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PubMed Services Nucleotide sequence specifying the glycoprotein gene, gB, of herpes simplex virus type 1.

The nucleotide sequence thought to specify the glycoprotein gene, gB, of the KOS

Bzik DJ, Fox BA, DeLuca NA, Person S.

strain of herpes simplex virus type 1 (HSV-1) has been determined. A 3.1-kilobase (kb), viral-specified RNA was mapped to the left half of the BamHI-G fragment (0.345 to 0.399 map units). TATA, CAT-box, and possible mRNA start sequences characteristic of HSV-1 genes are found near 0.368 map units. The first available ATG codon is at 0.366 and the first in-phase chain terminator at 0.348 map units. It polyA-addition signal (AATAAA) occurs 17 nucleotides past the chain terminator. Translation of these sequences would yield a 100.3-kilodalton (kDa) polypeptide characterized by a 5' signal sequence, nine N-linked saccharide addition sites, a strongly hydrophobic membrane-spanning sequence, and a highly charged 3' cytoplasmic anchor sequence. Two mutants of KOS, tsJ12 and tsJ20, that are temperature-sensitive for viral growth and for the production of gB, have been physically mapped to 0.357 to 0.360 and 0.360 to 0.364 map units, respectively (DeLuca et al., in preparation). The nucleotide sequence of the mutants was

determined in these regions. In both cases a single amino acid replacement within

the 100.3-kDa polypeptide is predicted from the sequence analysis.

Related Resources

MeSH Terms:

- Amino Acid Sequence
- Base Sequence
- Cell Line
- DNA Restriction Enzymes
- DNA, Recombinant/analysis
- Genes, Structural*
- · Genes, Viral*
- Human
- Lung/embryology
- Nucleic Acid Hybridization
- Simplexvirus/genetics*
- Support, Non-U.S. Gov't
- Support, U.S. Gov't, P.H.S.

Substances:

- DNA Restriction Enzymes
- DNA, Recombinant

Secondary source id:

• GENBANK/K01760

PMID: 6324454 [PubMed - indexed for MEDLINE]



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3 of 4

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    9481 cgaaggettt tgcattgtaa agetaccege ctaccegege eteccaataa aaaaagaaca
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    9601 teceatggta ecaaagaeeg gggegaatea gegggeeeee ateatetgag agaegaaeaa
    9661 atcggcggcg cgggccgtgt caacgtccac gtgtgctgcg ctgctggcgt tgacaagggc
    9721 cccggcctcc gcgttggatg cctccggttg ggatcc
11
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Revised: October 24, 2001.

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